We claim:

1. A computerized method for designing a resequencing array to resequence a user selected sequence comprising:

receiving a user design request comprising a user selected sequence;

5 producing an array design for resequencing said user selected sequence;

outputting said array design to said user;

receiving acceptance for said array design from said user;

outputting a file that is useful for controlling a nucleic acid synthesizer during the construction of an array comprising said array design;

synthesizing at least one copy of said array; and providing said at least one copy of said array to said user.

- 2. The method of claim 1 wherein said nucleic acid synthesizer is maskless.
- 15 3. The method of claim 1 wherein said user design request comprises a sequence file.
 - 4. The method of claim 1 wherein said user design request is received over the internet.
 - 5. The method of claim 1 wherein the array further comprises user selected control probes.

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6. A method for a provider of nucleic acid arrays to provide a user with an array for resequencing a user selected nucleic acid wherein the method comprises:

receiving a sequence computer file from said user wherein the sequence computer file comprises the sequence of the user selected nucleic acid;

25 preparing a design for a resequencing array for the selected sequence;

outputting said design into a design computer file;

providing said design computer file to said user;

receiving approval for said design from said user;

outputting an instruction computer file wherein said instruction computer file provides

30 instructions to a nucleic acid synthesizer for synthesis of an array comprising said design;

synthesizing said array; and

providing said user with said array.

7. The method of claim 6 wherein after receiving from said user said sequence computer file the provider analyzes the sequence to remove repetitive sequences.

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- 8. The method of claim 6 wherein said provider identifies ambiguous sequence within said user selected nucleic acid sequence by: obtaining analogous sequence from at least one other source; comparing the sequence from said file to said sequence from at least one other source; identifying bases that are different and removes ambiguity by comparing the sequence from two or more sources.
- 9. The method of claim 6 wherein said provider provides said user with computer executable code for identifying ambiguous sequence within a selected sequence and for resolving the ambiguity of the identified ambiguous sequence.

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- 10. The method of claim 6 wherein said provider also provides said user with the sequence of primers that may be used to amplify said user selected sequence.
- 11. The method of claim 10 wherein said provider further provides a graphical user interface for said user to order primers with the provided sequence from a third party on the internet.
 - 12. The method of claim 6 wherein said user selected sequence is identified by said user in an association study or a linkage study wherein said sequence is associated with a phenotype.
- 25 13. The method of claim 6 wherein said user first identifies said user selected sequence as being associated with a phenotype using a genotyping array that genotypes more than 10,000 different human polymorphisms.
- 14. The method of claim 6 wherein said sequence computer file is received by the provider over the Internet.

- 15. The method of claim 6 wherein said design computer file is provided to the user over the Internet.
- 16. A method for providing resequencing arrays to a user comprising:
- 5 using a computer to design one or more resequencing arrays for one or more regions of a genome of interest;

providing users with a list of available designs for resequencing arrays; receiving an order from a user for a specific design from said list of available designs

wherein said specific design is for an array to resequence a selected sequence; outputting an instruction computer file for said specific design to a nucleic acid

synthesizing an array using said instruction computer file; and providing the array or arrays to said user.

- 15 17. The method of claim 16 further comprising providing primer sequences to the user, wherein said primer sequences may be used to amplify at least one region of said selected sequence.
 - 18. The method of claim 16 wherein said genome of interest is the human genome.
 - 19. The method of claim 16 wherein said selected sequence comprises at least one complete chromosome.
- 20. The method of claim 16 wherein said list of available designs is provided to said user25 over the Internet.

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synthesizer;